## AMENDMENTS TO THE CLAIMS

Claims 1-27. (canceled).

Claim 28. (currently amended) A method for detecting a target nucleotide sequence, and providing a partial helical enclosure of the target sequence, comprising the steps of:

(a) rendering the target nucleotide sequence substantially single-stranded;

(b) hybridizing the single-stranded target nucleotide sequence with a nucleic acid probe unit, comprising : (i) a sequence complementary to the single-stranded target nucleotide sequence, and (ii) a probe linker at each of the two terminal ends of the probe unit, said probe linker comprises a single-stranded nucleotide sequence that hybridizes to a reporter linker of a reporter but does not hybridize to the single-stranded target nucleotide sequence;

(c) washing to remove any unbound probe;

(d) hybridizing reporters to the two probe linkers; and

(e) detecting the presence of the reporter to indicate the presence of the target nucleotide sequence.

Claim 29. (previously presented) The method of claim 28, wherein the probe unit comprises a first oligonucleotide comprising a sequence complementary to the single-stranded target nucleotide sequence flanked by a first probe linker on one end and an overlap linker on the other end, said overlap linker is hybridized to a second oligonucleotide comprising a second probe linker.

Claim 30. (previously presented) The method of claim 28, wherein the reporter comprises a labeled, double-stranded polynucleotide sequence linked

on one or both ends to a reporter linker that comprises a short single-stranded polynucleotide.

Claim 31. (previously presented) The method of claim 30, wherein the double-stranded polynucleotide sequence is at least 100 bases long and the short single-stranded polynucleotide linker is from about 20 bases to about 30 bases long.

Claim 32. (previously presented) The method of claim 30, wherein two or more reporters form a reporter array by linking end-to-end via the reporter linker.

Claim 33. (previously presented) The method of claim 32, wherein the length of the reporter array is determined by a ratio of terminator oligonucleotide to reporters, said terminator oligonucleotide terminates the reporter array by hybridizing to a reporter linker at the end of the reporter array.

Claim 34. (currently amended) The method of claim 32, wherein the reporter array comprises successive layers of type I and type II reporters, each of the type I and type II reporter comprises a first and a second reporter linker, wherein the first and the second reporter linker of a type I reporter is hybridized respectively to the second reporter linker of a type II reporter and to the first reporter linker of another type II reporter, except the first reporter linker of the type I reporter in the first layer of reporter is hybridized to a probe linker of a probe.

Claim 35. (previously presented) The method of claim 28, wherein a multi-linking unit is interposed between the reporter and the probe linker, said multi-linking unit comprises (i) a sequence that hybridizes to the probe linker and (ii) two or more sequences that hybridize to the reporter linker of the reporter.

Claims 36-58. (canceled).

Claim 59. (currently amended) The method of claim 29, wherein the overlap linker and or the probe linker comprises one or more TA sequence to facilitate interstrand crosslinking between complementary linkers during probe fabrication or use.

Claim 60. (original) The method of claim 30, wherein the reporter linker comprises a carbon spacer segment.

Claim 61. (currently amended) The method of claim 30, wherein the reporter linker comprises sequence selected from the group consisting of SEQ ID NO. 6, 10, 12, 71, 73, 76, 78 ~~and~~ 81 and 83.